

P65#26 -> Genes
DNA sequence 1665 b.p. gaattcggttc ... caagccgaattc linear

P60-1

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1  i gaattcggttc ATG GCG GCT AAA GAC GTA AAA TTC GGT AAC GAC GCT CGT GTG AAA ATG CTG CGC GGC GTA AAC 77
   M A A K D V K F G N D A R V K M L R G V N 21

78 GTA CTG GCA GAT GCA GTG AAA GTT ACC CTC GGC CCA AAA GGC CGT AAC GTA GTT CTG GAT AAA TCT TTC GGT GCA 152
22 V L A D A V K V T L G P K G R N V V L D K S F G A 46

153 CCG ACC ATC ACT AAA GAT GGT GTT TCC GTA GCA CGT GAA ATC GAA CTG GAA GAC AAG TTC GAA AAC ATG GGT GCG 227
47 P T I T K D G V S V A R E I E L E D K F E N M G A 71

228 CAG ATG GTG AAA GAA GTT GCC TCT AAA GCG AAC GAC GCT GCA GGT GAC GGT ACC ACC GCA ACC GTA CTG GCT 302
72 Q M V K E V A S K A N D A A G D G T T A T V L A 96

303 CAG TCC ATC ATC ACT GAA GGC CTG AAA GCC GTT GCT GCG GGC ATG AAC CCG ATG GAT CTG AAA CGT GGT ATC GAC 377
97 Q S I I T E G L K A V A A G M N P M D L K R G I D 121

378 AAA GCT GTC GCT GCT GCT GAA GAA CTG AAA GCA CTG TCC GTA CCG TGC TCC GAC TCT AAA GCT ATT GCT CAG 452
122 K A V A A A V E E L K A L S V P C S D S K A I A Q 146

453 GTT GGT ACC ATC TCC GCT AAC TCC GAC GAA ACC GTA GGT AAA CTG ATC GCT GAA GCG ATG GAC AAA GTC GGT AAA 527
147 V G T I S A N S D E T V G K L I A E A M D K V G K 171

528 GAA GGC GTG ATC ACC GTT GAA GAC GGT ACC GGT CTG CAG GAC GAA CTG GAC GTG GTT GAA GGT ATG CAG TTC GAC 602
172 E G V I T V E D G T G L Q D E L D V V E G M Q F D 196

603 CGT GGC TAC CTG TCT CCT TAC TTC ATC AAC AAG CCG GAA ACT GGC GCA GTA GAA TTG GAA AGC CCG TTC ATC CTG 677
197 R G Y L S P Y F I N K P E T G A V E L E S P F I L 221

678 CTG GCT GAC AAG AAA ATC TCC AAC ATC CGC GAA ATG CTG CCG GTT CTG GAA GCT GTA GCG AAA GCA GGC AAA CCG 752
222 L A D K K I S N I R E M L P V L E A V A K A G K P 246

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FIG. 1A



753 CTG CTG ATC ATC GCT GAA GAT GTT GAA GGC GAA GCG CTG GCA ACT CTG GTT GTT AAC ACC ATG CGC GGT ATC GTA 827
247 L I I A E D V E G A L A T L V V N T M R G I V 271

828 AAA GTC GCT GCG GTT AAA GCA CCT GGC TTC GGC GAT CGT CGT AAA GCA ATG CTG CAG GAT ACC CTG ACC 902
272 K V A A V K A P G F G D R R K A M L Q D I A T L T 296

903 GGT GGT ACC GTT ATC TCT GAA GAG ATC GGT ATG GAG CTG GAA AAA GCA ACT CTG GAA GAT CTG GGC CAG GCG AAA 977
297 G T V I S E I G M E L E K A T L E D L G Q A K 321

978 CGC GTT GTT ATC AAC AAA GAT ACC ACC ATC ATC GAT GGC GTG GGC GAC GAA GCT GCA ATC CAG GGT CGC GTG 1052
322 R V V I N K D T T I I I D G V G D E A A I Q G R V 346

1053 ACT CAG ATT CGT CAG CAG ATC GAA GCA ACT TCC GAC TAT GAC CGT GAA AAA CTG CAG GAG CGC GTA GCG AAA 1127
347 T Q I R Q Q I E A T S D Y D R E K L Q E R V A K 371

1128 CTG GCA GGC GTT GCG GTT ATC AAA GTT GGT GCT GCG ACT GAA GTT GAA ATG AAA GAG AAG AAA GCC CGC GTT 1202
372 L A G G V A V I K V G A A T E V E M K E K A R V 396

1203 GAA GAT GCC CTG CAC GCT ACC CGT GCT GCG GTA GAA GGC GTG GTT GCT GGT GGC GTT GCG CTG ATT CGC 1277
397 E D A L H A T R A A V E E G V V A G G G V A L I R 421

1278 GTA GCG TCT AAA ATT GCC GGC CTG AAA GGT CAG AAC GAA GAC CAG AAC GTA GGT ATC AAA GTT GCG CTG CGC GCA 1352
422 V A S K I A G L K G Q N E D Q N V G I K V A L R A 446

1353 ATG GAA TCC CCA CTG CGT CAA ATC GTA CTG AAC TGC GGC GAA GAG CCG TCT GTA GTG GCT AAC ACC GTG AAA GCC 1427
447 M E S P L R Q I V L N C G E E P S V V A N T V K A 471

1428 GGT GAC GGT AAC TAC GGT TAC AAC GCT GCA ACT GAA GAA TAC GGC AAC ATG ATC GGT ATC CTG GAT CCA 1502
472 G D G N Y G Y N A A T E E Y G N M I D M G I L D P 496

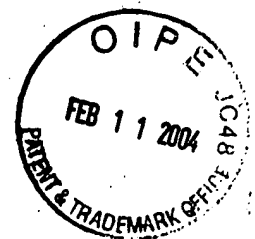
1503 ACC AAA GTA ACT CGT TCT GCT CTG CAG TAC GCG GCT TCT GTT GCG GGT CTG ATG ATC ACC ACC GAG TGC ATG GTT 1577
497 T K V T R S A L Q Y A A S V A G L M I T T E C M V 521

1578 ACC GAC CTG CCG AAA GGC GAT GCA CCT TTA GGT GCT GCT GGT ATG GGC GGC ATG GGC GGA ATG ATG TGA 1652
522 T D L P K G D A P D L G A A G G M G G M G M M * 546

1653 tcaagccgaactc

1665

FIG. 1B



P65#44 -> Genes

DNA sequence 1654 b.p. gaattcggttc ... aaagccgaattc linear
use to subclone for expression

P60-2

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  1 M A K E I K F S S D A R S A M V R G V D I 21

78 CTT GCA GAT ACT GTT AAA GTA ACT TTG GGA CCA AAA GGT CGC AAT GTC GTT CTT GAA AAG TCA TTC GGT TCA CCC 152
  22 L A D T V K V T L G P K G R N V V L E K S F G S P 46

153 TTG ATT ACC AAT GAC GGT GTG ACT ATT GCC AAA GAA ATT GAA TTA GAA GAC CAT TTT GAA AAT ATG GGT GCC AAA 227
  47 L I T N D G V T I A K E I E L E D H F E N M G A K 71

228 TTG GTA TCA GAA GTA GCT TCA AAA ACC AAT GAT ATC GCA GGT GAT GGA ACT ACA ACT GCA ACT GTT TTG ACC CAA 302
  72 L V S E V A S K T N D I A G D G T T A T V L T Q 96

303 GCA ATC GTC CGT GAA GGA ATC AAA AAC GTC ACA GCA GGT GCA AAT CCA ATC GGT GGG ATT GAA ACA 377
  97 A I V R E G I K N V T A G A N P I G I R R G I E T 121

378 GCA GTT GCC GCA GCA GTT GAA GCT TTG AAA AAC AAC GTC ATC CCT GTT GCC AAT AAA GAA GCT ATC GCT CAA GTT 452
  122 A V A A A V E A L K N N V I P V A N K E A I A Q V 146

453 GCA GCC GTA TCT TCT CGT TCT GAA AAA GTT GGT GAG TAC ATC TCT GAA GCA ATG GAA AAA GTT GGC AAA GAC GGT 527
  147 A A V S S R S E K V G E Y I S E A M E K V G K D G 171

528 GTC ATC ACC ATC GAA GAG TCA CGT GGT ATG GAA ACA GAG CTT GAA GTC GTA GAA GGA ATG CAG TTT GAC CGT GGT 602
  172 V I T I E S R G M E T E L E V V E G M Q F D R G 196

603 TAC CTT TCA CAG TAC ATG GTG ACA GAT AGC GAA AAA ATG GTG GCT GAC CTT GAA AAT CCG TAC ATT TTG ATT ACA 677
  197 Y L S Q Y M V T D S E K M V A D L E N P Y I L I T 221

678 GAC AAG AAA ATT TCC AAT ATC CAA GAA ATC TTG CCA CTT TTG GAA AGC ATT CTC CAA AGC AAT CGT CCA CTC TTG 752
  222 D K K I S N I Q E I L P L L E S I L Q S N R P L L 246

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FIG. 2A





753 ATT ATT GCG GAT GAT GTG GAT GGT GAG GCT CTT CCA ACT CTT GTT TTG AAC AAG ATT CGT GGA ACC TTC AAC GTA 827
247 I I A D V D G E A L P T L V L N K I R G T F N V 271

828 GTA GCA GTC AAG GCA CCT GGT TTT GGT GAC CGT CGC AAA GCC ATG CTT GAA GAT ATC GCC ATC TTA ACA GGC GGA 902
272 V A V K A P G F G D R R K A M L E D I A I L T G G 296

903 ACA GTT ATC ACA GAA GAC CTT GGT CTT GAG TTG AAA GAT GCG ACA ATT GAA GCT CTT GGT CAA GCA GCG AGA GTG 977
297 T V I T E D L G L E L K D A T I E A L G Q A A R V 321

978 ACC GTG GAC AAA GAT AGC AGT ATT GTA GAA GGT GCA GGA AAT CCT GAA GCG ATT TCT CAC CGT GTT GCG GTT 1052
322 T V D K D S T V I V E G A G N P E A I S H R V A V 346

1053 ATC AAG TCT CAA ATC GAA ACT ACA ACT TCT GAA TTT GAC CGT GAA AAA TTG CAA GAA CGC TTG GCC AAA TTG TCA 1127
347 I K S Q I E T T T S E F D R E K L Q E R L A K L S 371

1128 GGT GGT GTA GCG GTT ATT AAG GTC GGA GCC GCA ACT GAA ACT GAG TTG AAA GAA ATG AAA CTC CGC ATT GAA GAT 1202
372 G G V A V I K V G A A T E T E L K E M K L R I E D 396

1203 GCC CTC AAC GCT ACT CGT GCA GCT GTT GAA GAA GGT ATT GTT GCA GGT GGT GGA ACA GCT CTT GCC AAT GIG ATT 1277
397 A L N A T R A A V E E G I V A G G T A L A N V I 421

1278 CCA GCT GTT GCT ACC TTG GAA TTG ACA GGA GAT GAA GCA ACA GGA CGT AAT ATT GTT CTC CGT GCT TTG GAA GAA 1352
422 P A V A T L E L T G D E A T G R N I V L R A L E E 446

1353 CCT GTT CGT CAA ATT GCT CAC AAT GCA GGA TTT GAA GGA TCT ATC GTT ATC GAT CGT TTG AAA AAT GCT GAG CTT 1427
447 P V R Q I A H N A G F E G S I V I D R L K N A E L 471

1428 GGT ATA GGA TTC AAC GCA ACT GGC GAG TGG GTT AAC ATG ATT GAT CAA GGT ATC ATT GAT CCA GTT AAA GTG 1502
472 G I G F N A A T G G E W V N M I D Q G I I D P V K V 496

1503 AGT CGT TCA GCC CTA CAA AAT GCA GCA TCT GTA GCC AGC TTG ATT TTG ACA ACA GAA GCA GTC GTA GCC AAT AAA 1577
497 S R S A L Q N A A S V A S L I L T T E A V V A N K 521

1578 CCA GAA CCA GTA GCC CCA GCT CCA GCA ATG GAT CCA AGT ATG GGT GGA ATG GGC GGA TGA ccaaagccgaattc 1654
522 P E P V A P A P A M D P S M M G G G * 542

FIG. 2B



Y65#5 -> Genes
DNA sequence 1662 b.p. gaattcggcttc ... caagccgaattc linear

Y60-1

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1 M A A K D V K F G N D A R V K M L R G V N 21

78 GTA CTG GCA GAC GCA GTT AAA GAT ACC CTG GGC CCG AAA GGC CGT AAC GTA GTG CTG GAC AAA TCC TTC GGC GCG 152
22 V L A D A V K V T L G P K G R N V V L D K S F G A 46

153 CCA ACC ATC ACG AAA GAT GGT GTT TCT GTA GCA CGT GAA ATC GAG CTG GAA GAC AAG TTC GAA AAC ATG GGC GCG 227
47 P T I T K D G V S V A R E I E L E D K F E N M G A 71

228 CAG ATG GTG AAA GAA GTG GCC TCT AAA GCG AAC GAC GCT GCA GGC GAC GGT ACC ACC GCG ACC GTG CTG GCT 302
72 Q M V K E V A S K A N D A A G D G T T A T V L A 96

303 CAG GCT ATC ATC ACC GAA GGT CTG AAA GCC GTT GCT GCG GGC ATG AAC CCA ATG GAT CTG AAA CGT GGT ATC GAC 377
97 Q A I I T E G L K A V A A G M N P M D L K R G I D 121

378 AAA GCT GTC GCG TCC GCT GTT GAA GAA CTG AAA GCG CTG TCC GTA CCG TGC TCT GAC TCT AAA GCC ATT GCT CAG 452
122 K A V A S A V E L K A L S V P C S D S K A I A Q 146

453 GTA GGT ACC ATC TCC GCT AAC TCC GAC GAA ACC GTA GGT AAA CTG ATC GCG GAA GCG ATG GAT AAA GTC GGT AAA 527
147 V G T I S A N S D E T V G K L I A E A M D K V G K 171

528 GAA GGC GTG ATC ACC GTT GAA GAC GGT ACC GGT CTG GAA GAC GAA CTG GAC GTG GTT GAA GGT ATG CAG TTC GAC 602
172 E G V I T V E D G T G L E D E L D V V E G M Q F D 196

603 CGC GGT TAC CTG TCC CCA TAC TTC ATC AAC AAG CCA GAA ACT GGC GCT GTT GAG CTG GAA AGC CCG TTC ATC CTG 677
197 R G Y L S P Y F I N K P E T G A V E L E S P F I L 221

678 CTG GCT GAC AAG AAA ATC TCC AAC ATC CGC GAA ATG CTG CCA CTG GAA GCC GTT GCG AAA GCA GGC AAA CCG 752
222 L A D K K I S N I R E M L P V L E A V A K A G K P 246
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FIG. 3A



753 CTG GTT ATC ATT GCT GAA GAC GTT GAA GGC GAA GCG CTG GCG ACC CTG GTG GTT AAC ACC ATG CGT GGC ATC GTG 827
247 L V I I A E D V E G E A L A T L V V N T M R G I V 271

828 AAA GTG GCT GCG GTT AAA GCA CCT GGC TTC GGC GAC CGC CGT AAA GCG ATG CTG CAG GAT ATC GCT ACC CTG ACC 902
272 K V A A V K A P G F G D R R K A M L Q D I A T L T 296

903 GGC GGT ACC GTC ATC TCT GAA GAG ATC GGT ATG GAG CTG GAA AAA GCG ACC CTG GAA GAC CTG GGC CAG GCT AAA 977
297 G G T V I S E E I G M E L E K A T L E D L G Q A K 321

978 CGT GTT GTG ATC AAC AAA GAC ACC ACC ATC ATC ATC GAT GGC GTG GGC GAC GAA GCG GCG ATT CAG GGC CGT GTT 1052
322 R V V I N K A A A GAC ACC ACC T T T I I D G V G D E A A I Q G R V 346

1053 GGT CAG ATC CGT AAG CAG ATC GAA GAA GCC ACT TCC GAT TAC GAC CGT GAA AAA CTG CAG GAG CGC GTA GCG AAA 1127
347 G Q I R K Q I E E A T S D Y D R E K L Q E R V A K 371

1128 CTG GCA GGC GGT GTT GCG GTA ATC AAA GTC GGT GCT GCG ACT GAA GTT GAA ATG AAA GAG AAA GCA CGC GTT 1202
372 L A G G V A V I K V G A T E V E M K E K A R V 396

1203 GAC GAT GCC CTG CAC GCG ACC CGT GCT GCG GTA GAA GGC GTG GTT GGT GGT GCG CTG GCG CTG GTG CGT 1277
397 D A L H A T R A A V E E G V V A G G V A L V R 421

1278 GTT GCC GCG AAA CTG TCC GGC CTG ACT GCT CAG AAC GAA GAT CAG AAC GTG GGT ATC AAA GTT GCG CTG CGC GCA 1352
422 V A A K L S G L T A Q N E D Q N V G I K V A L R A 446

1353 ATG GAA GCT CCA CTG CGT CAG ATC GTG TCC AAC GCC GGT GAA GAG CCA TCT GTT GTG ACC AAC AAC GTG AAA GCA 1427
447 M E A P L R Q I V S N A G E E P S V V T N N V K A 471

1428 GGC GAA GGT AAC TAC GGT TAC AAC GCA ACT GAA GAA TAC GGC AAC ATG ATC GAC TTC GGT ATC CTG GAT CCA 1502
472 G E G N Y G Y N A A T E E Y G N M I D F G I L D P 496

1503 ACC AAA GTG ACC CGT TCT GCT CTG CAG TAC GCG GCA TCT GTC GCT GGC CTG ATG ATC ACC ACC GAG TGC ATG GTG 1577
497 T K V T R S A L Q Y A A S V A G L M I T T E C M V 521

1578 ACC GAC CTG CCT AAA GGC GAC GCA CCT GAC TTA GGT GCT GCA GGC ATG GGT GGC GGT ATG ATG TGA tcaa 1653
522 T D L P K G D A P D L G A A G M G G M M * 545

1654 gccgaattc 1662

FIG. 3B



Y65#21 -> Genes
 DNA sequence 1661 b.p. gaattcggttc ... TAAGccgaattc linear
 V261 - same in clone Y65#24, too
 used to subclone for expression !!!

Y60-2

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  M A K E I K F S A D A R A A M V R G V D M 21

78 TTA GCA GAT ACC GTC AAA GTA ACG CTT GGT CCT AAA GGG CGC AAT GTT GTT CTT GAA AAA GCT TTT GGT TCT CCC 152
22 L A D T V K V T L G P K G R N V V L E K A F G S P 46

153 TTA ATT ACT AAT GAC GGG GTA ACC ATT GCT AAA GAG ATC GAA TTA GAA GAT CAT TTT GAA AAC ATG GGA GCA AAA 227
47 L I T N D G V T I A K E I E L E D H F E N M G A K 71

228 TTG GTG TCT GAA GTG GCT TCT AAA ACC AAT GAT ATT GCT GGT GAT GGG ACG ACT ACT GCA ACA GTT TTG ACA CAA 302
72 L V S E V A S K T N D I A G D G T T A T V L T Q 96

303 GCC ATT GTT CAT GAA GGA GGA CTA AAA AAT GTG ACA GGT GCT AAT CCA ATT GGT ATC CGT CGA GGC ATT GAA ACA 377
97 A I V H E G L K N V T A G A N P I G I R G I E T 121

378 GCA ACA GCA ACA GCT GTT GAA GCC TTG AAA GCC ATT GCT CAA CCT GTA TCT GGC AAG GAA GCT ATT GCT CAG GTC 452
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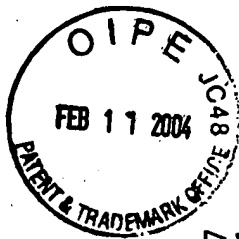
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528 GTG ATT ACC ATC GAA GAA TCT CGA GGT ATG GAA ACA CTT GAA GTG GTT GAA GGC ATG CAA TTT GAC CGT GGT 602
172 V I T I E E S R G M E T E L E V V E G M Q F D R G 196

603 TAC CTG TCT CAA TAC ATG GTC ACA GAC AAT GAA AAA ATG GTT GCA GAC CTT GAA AAC CCA TTT ATC TTA ATC ACG 677
197 Y L S Q Y M V T D N E K M V A D L E N P F I L I T 221

678 GAT AAA AAA GTG TCA AAC ATC CAA GAC ATT TTG CCA CTA CTT GAG GAA GTT CTT AAA ACC AAC CGT CCA TTA CTC 752
222 D K K V S N I Q D I L L P L L E E V L K T N R P L L L 246
  
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FIG. 4A



753 ATT ATT GCA GAT GAT GTG GAT GGT GAA GCA CTT CCA ACC CTT GTC TTG AAC AAG ATT CGT GGT ACT TTC AAT GTG 827
247 I I A D D V D G E A L P T L V L N K I R G T F N V 271

828 GTT GCT GTC AAA GCG CCA GGA TTT GGT GAT CGT CGT AAA GCT ATG CTT GAA GAC ATT GCT ATC TTG ACA GGT GGT 902
272 V A V K A P G F G D R R K A M L E D I A I L T G G 296

903 ACA GTG ATT ACA GAG GAT CTA GGA CTT GAA TTA AAA GAT GCT ACA ATG ACA GCC CTT GGA CAG GCT GCT AAG ATT 977
297 T V I T E D L G L E L K D A T M T A L G Q A A K I 321

978 ACA GTT GAT AAA GAT AGC ACA GTA ATT GTT GAA GGT TCA GGA AGT TCA GAA GCT ATT GCT AAC CGT ATT GCA CTG 1052
322 T V D K D S T V I V E G S G S S E A I A N R I A L 346

1053 ATT AAA TCG CAA TTA GAA ACA ACA ACT TCT GAC TTT GAC GAA AAA CTA CAA GAA CGT TTG GCG AAA TTA GCT 1127
347 I K S Q L E T T T S D F D R E K L Q E R L A K L A 371

1128 GGT GGT GTA GCT GTT ATC AAA GTA GGA GCT CCA ACA GAG ACA GCT TTA AAA GAA ATG AAA CTT CGC ATT GAG GAT 1202
372 G G V A V I K V G A P T E T A L K E M K L R I E D 396

1203 GCT CTA AAT GCT ACA CGT GCA GCC GTT GAA GAA GGT ATC GCT GGT GGT GGA ACA GCA CTT ATT ACG GTT ATT 1277
397 A L N A T R A A V E E G I V A G G T A L I T V I 421

1278 GAA AAA GTA GCA GCT CTT GAG CTT GAG GGC GAT GAT GCT ACT GGA CGT AAC ATT GTG CTT CGT GCT CTA GAA GAG 1352
422 E K V A A L E L E G D A T G R N I V L R A L E E 446

1353 CCT GTA CGT CAA ATT GCT TTA AAT GCT GGG TAC GAA GGC TCC GTA GTT ATT GAC AAG TTG AAA AAC AGC CCT GCA 1427
447 P V R Q I A L N A G Y E G S V V I D K L K N S P A 471

1428 GGA ACA GGA TTT AAT GCT GCA ACA GGT GAG TGG GTT GAT ATG ATT AAA ACA GGA ATC ATT GAC CCT GTC AAA GTA 1502
472 G T G F N A A T G A T G E W V D M I K T G I I D P V K V 496

1503 ACA CGA TCA GCG CTT CAA AAT GCA GCT TCT GTA GCT AGT CTT ATT TTG ACA ACA GAA GCA GTT GCT AAT AAA 1577
497 T R S A L Q N A A S V A S L I L T T E A V V A N K 521

1578 CCT GAA CCA GCT ACG CCA GCG CCA GCA ATG CCA GGA ATG ATG GGT GGG ATG GGC GGA TAA 1652
522 P E P A T P A P A M P A G M M G G M G G G 546

1653 gccgaattc

1661

FIG. 4B



Sequencing strategy (scale : 1cm = approx. 100bp)

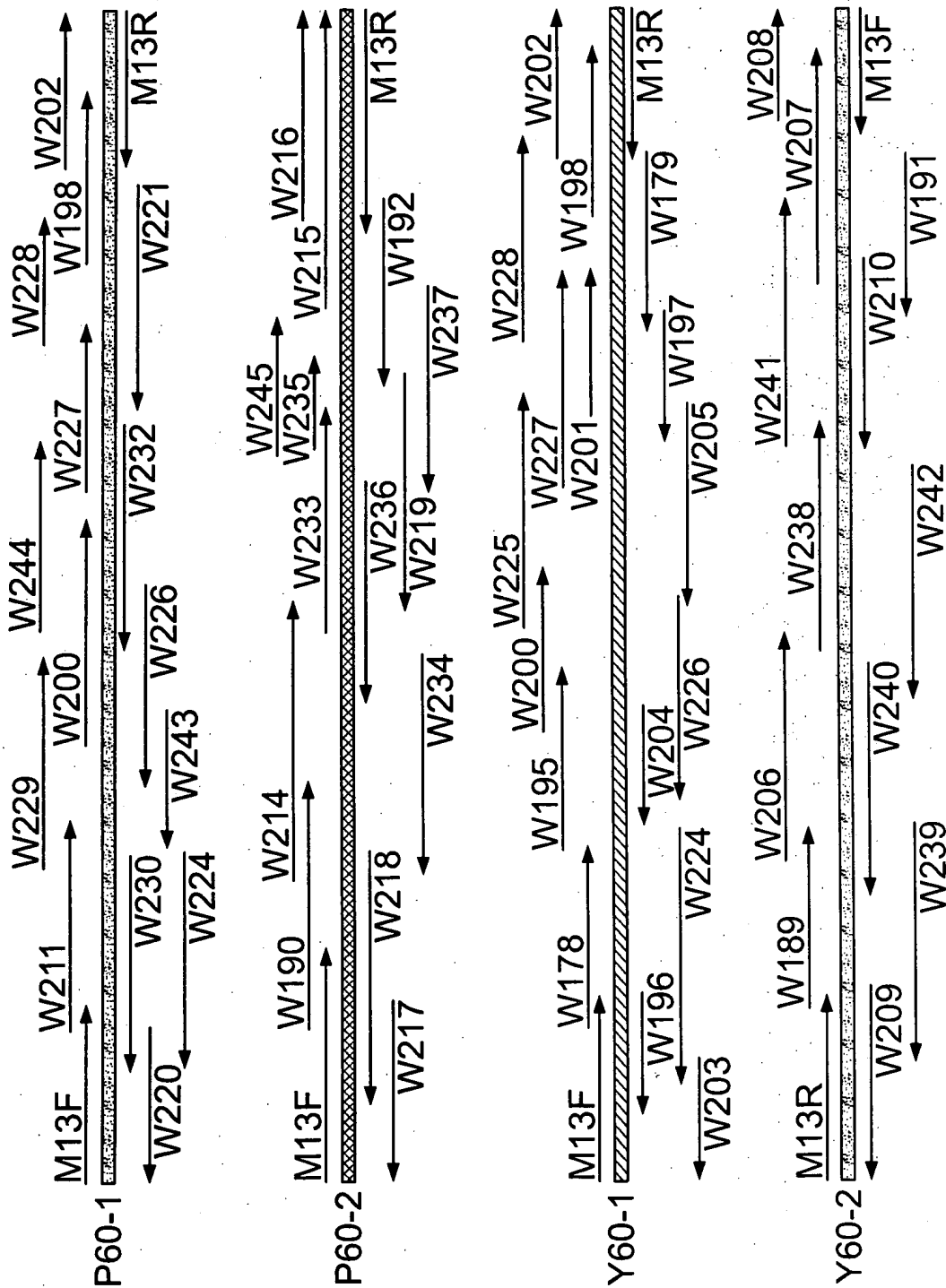


FIG. 5

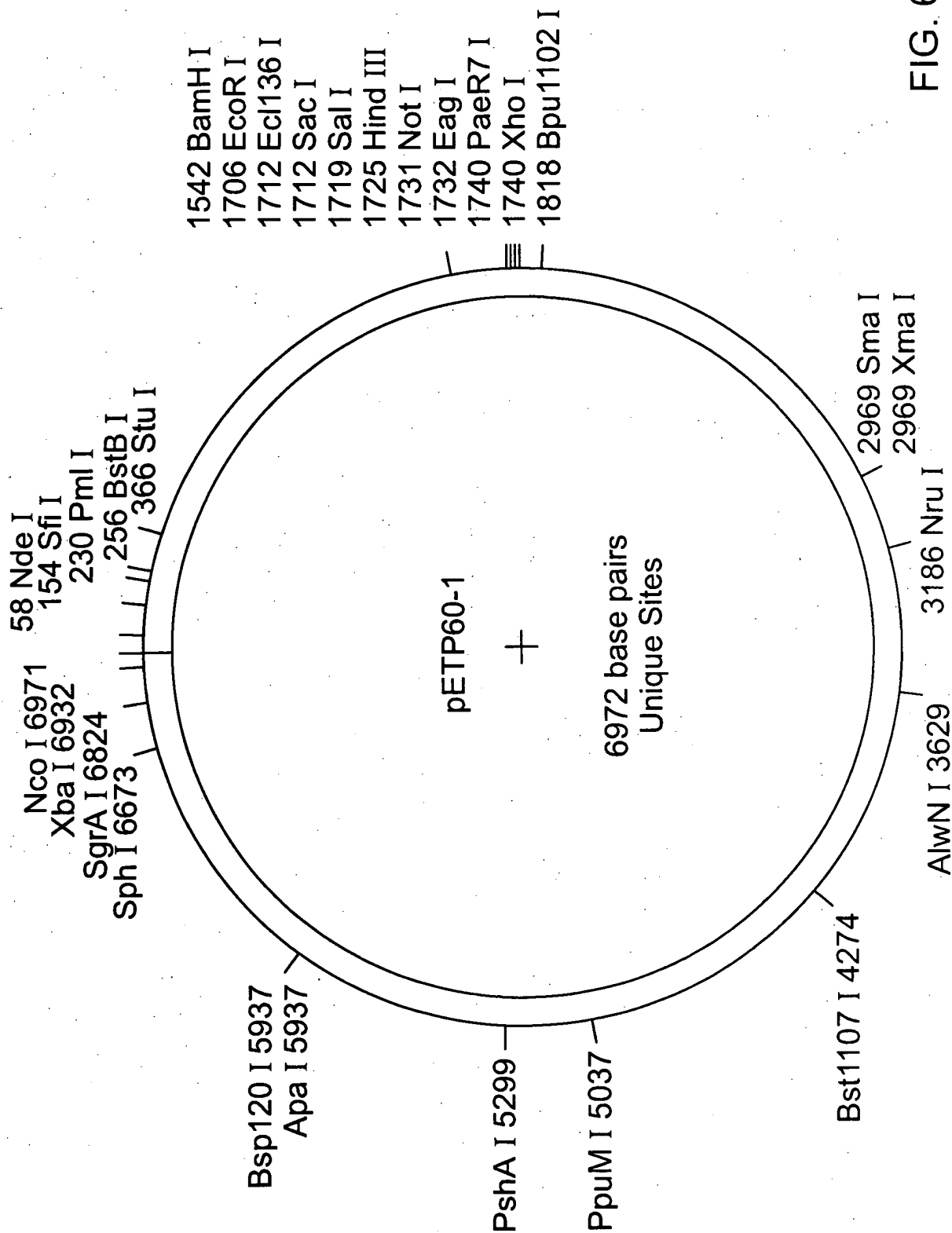


FIG. 6

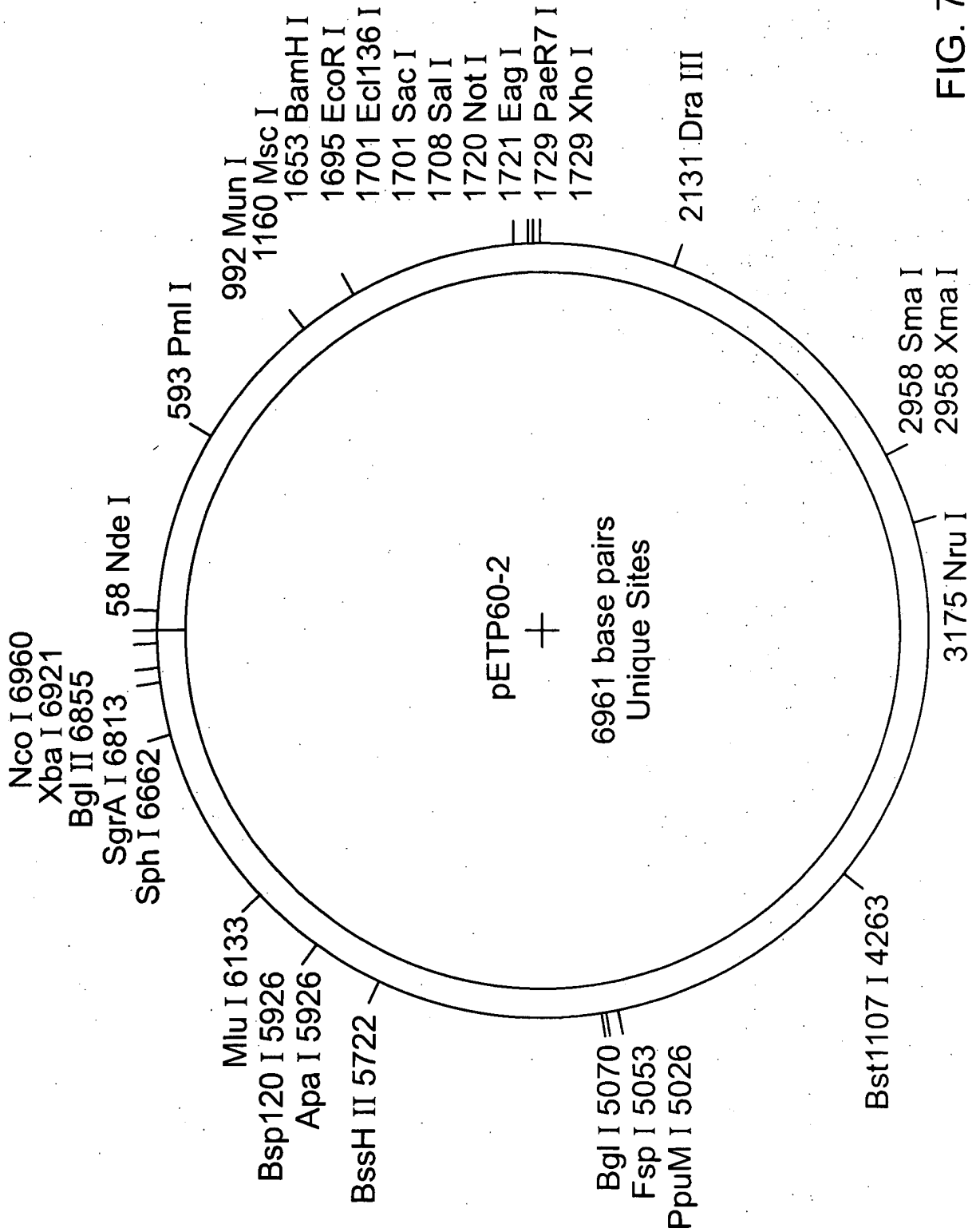


FIG. 7

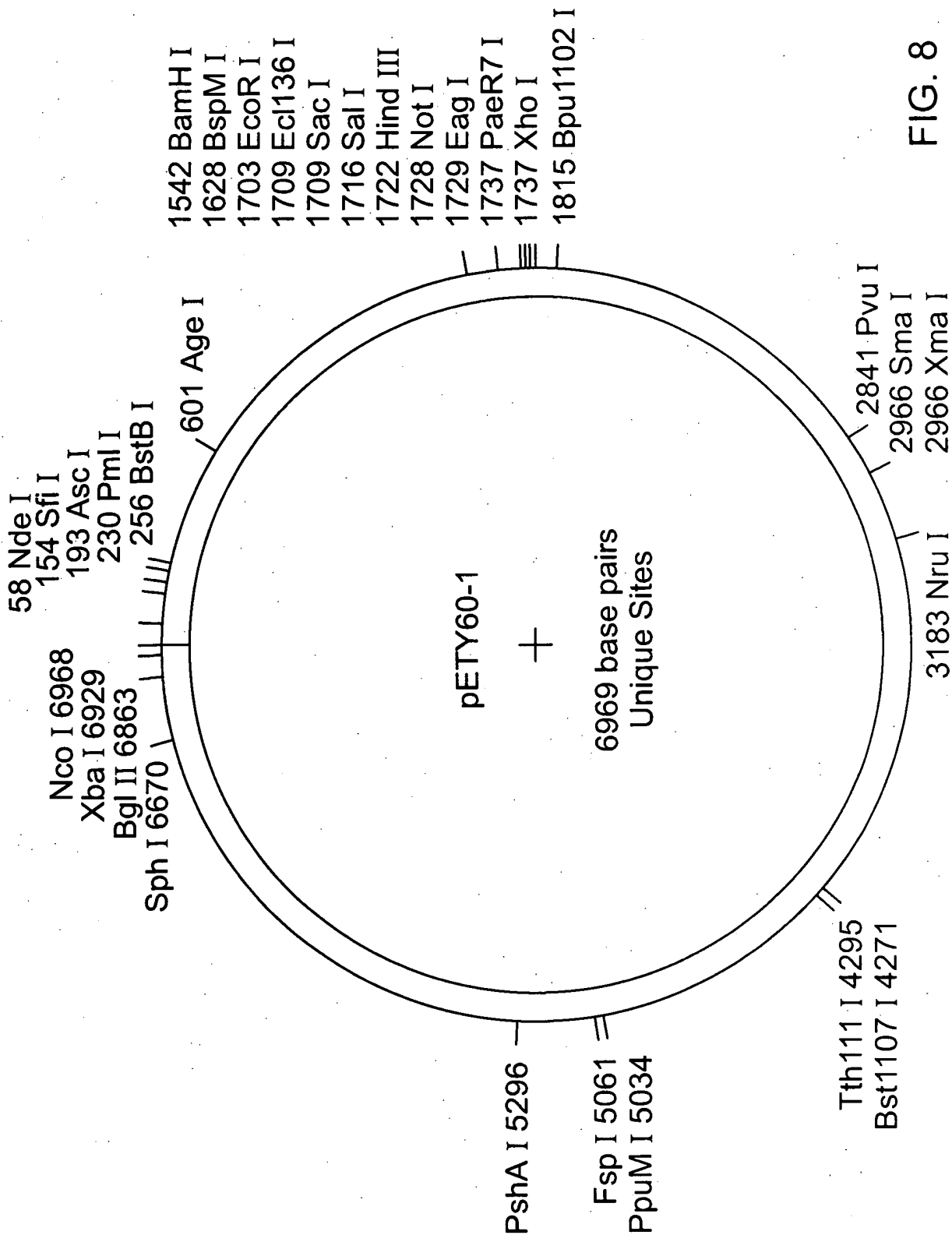
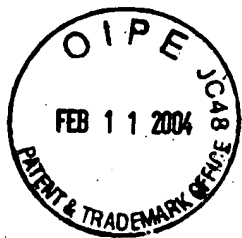


FIG. 8

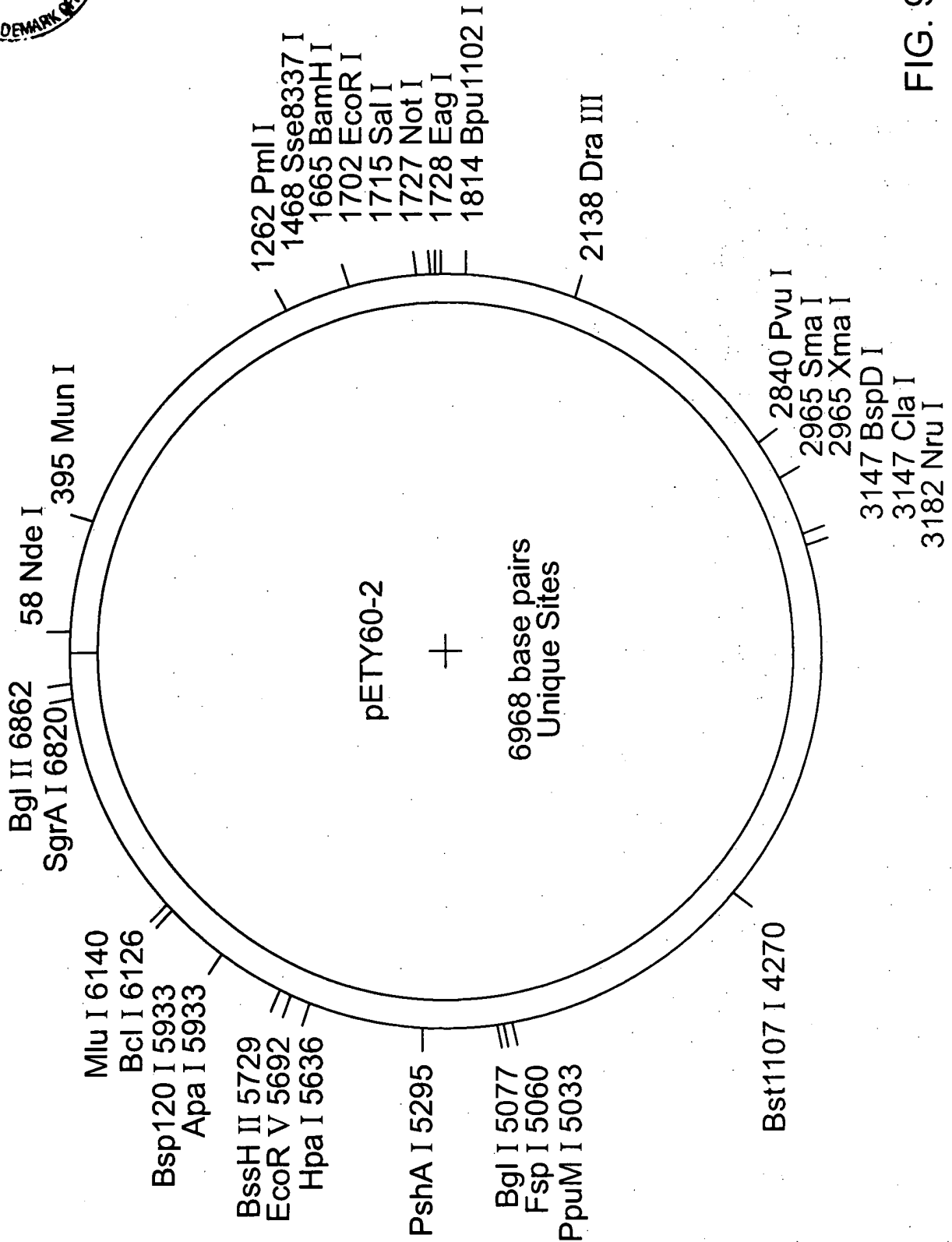


FIG. 9

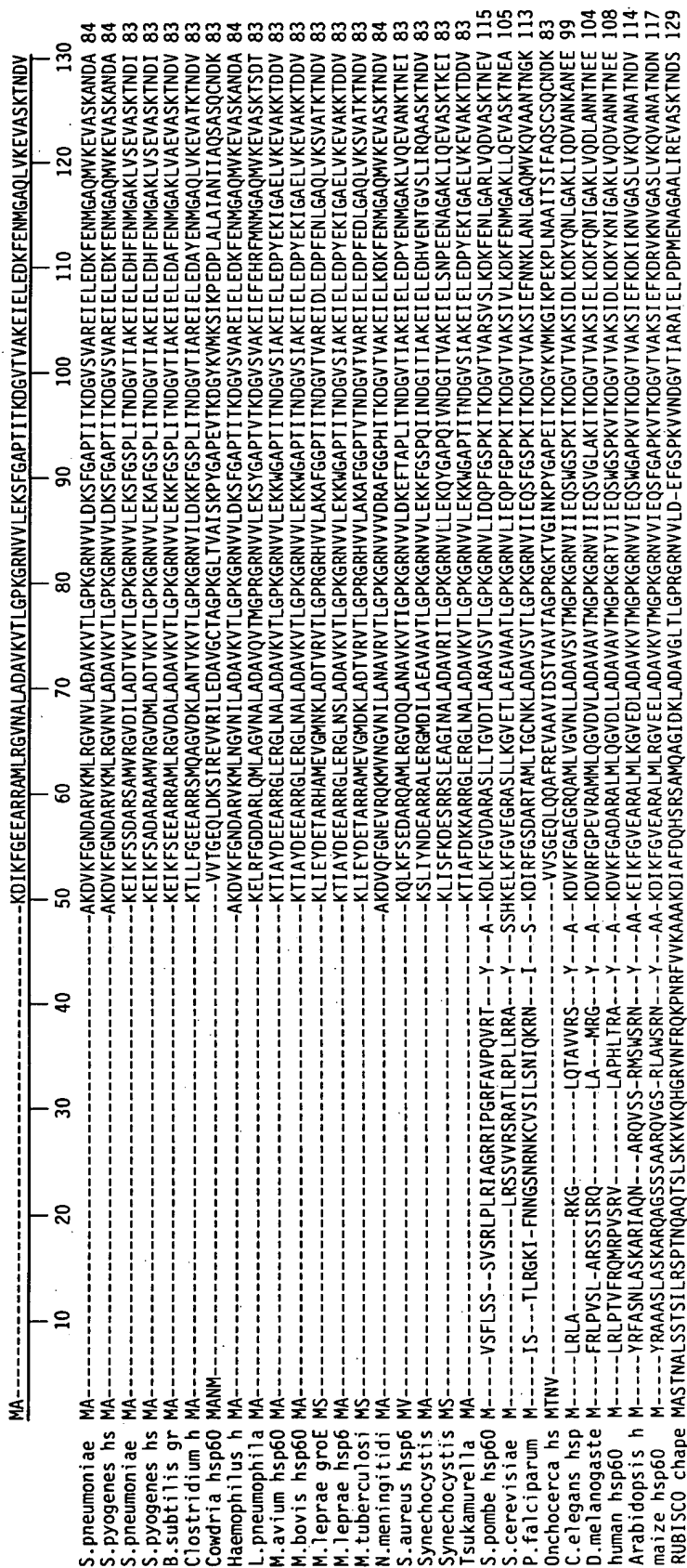


FIG. 10A

Page 15 of 19
STREPTOCOCCAL HEAT SHOCK PROTEINS OF THE HSP60 FAMILY
Lee Mizzen et al.
09/001,737
12071-014001

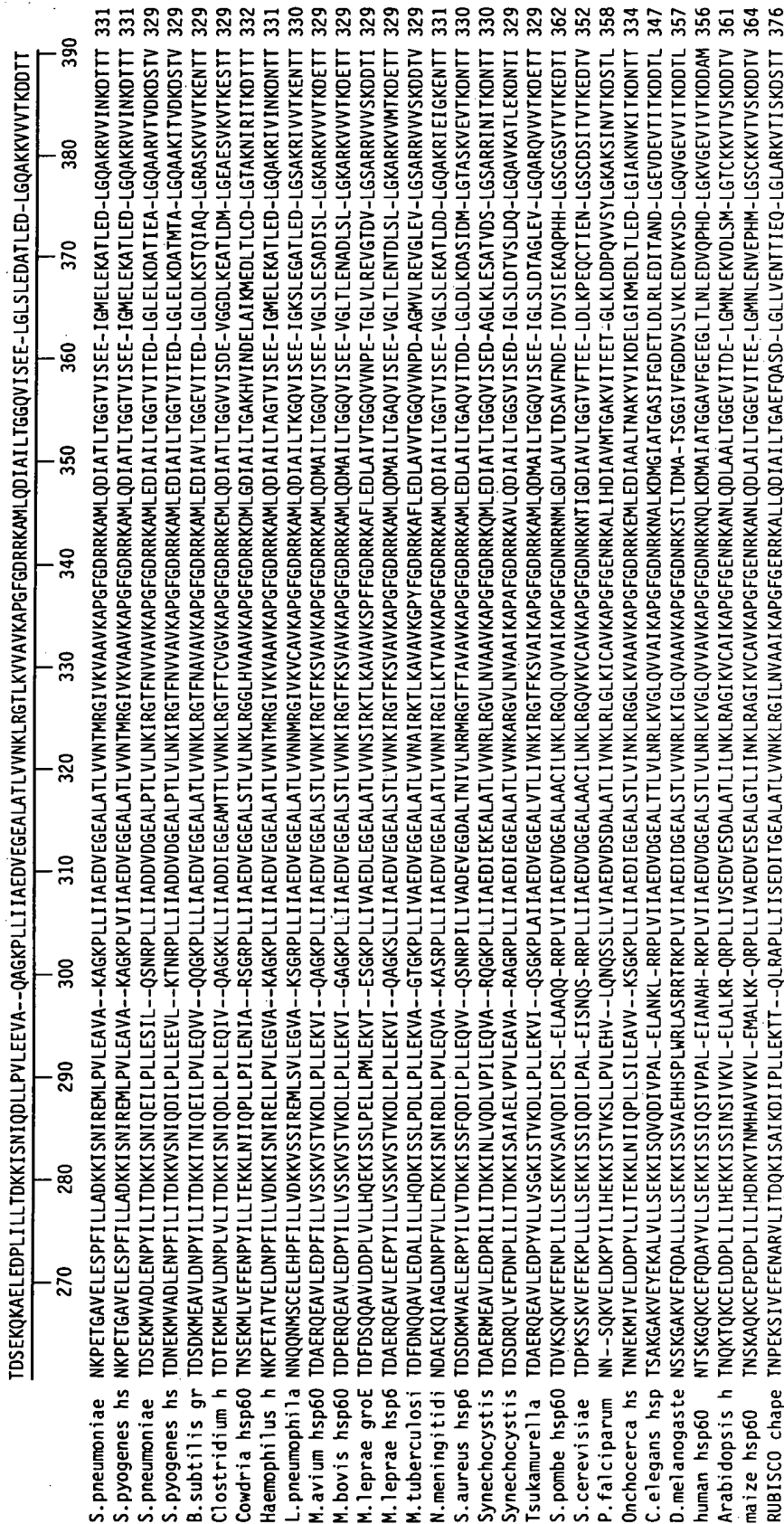


FIG. 10C



IVDAGD---AAIAGRVQIRSQIEEST--SDYDKEKLQERLAKLAGGVAVIKVGAATEVELKERRKORVEDALNATRAAVEEGIVPGGGVALLRAAPALDKLTE--NGDEATGVNIVLRALEAPLRQIAE
400 410 420 430 440 450 460 470 480 490 500 510 520
S. pneumoniae IIDGVGD---EAAIQGRVQIRSQIEEAT--SDYDREKLQERLAKLAGGVAVIKVGAATEVEHMEKKARVEDALHATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVL 456
S. pyogenes hs IIDGVGD---EAAIQGRVQIRSQIEEAT--SDYDREKLQERLAKLAGGVAVIKVGAATEVEHMEKKARVEDALHATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 456
S. pneumoniae IVEGAGN---PEATSHRVQIKSQIETT--SEFDREKLQERLAKLAGGVAVIKVGAATEVELKEMKLRIEDALNATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 453
S. pyogenes hs IVEGSGS---SEATANRIALIKSQIETT--SDFDREKLQERLAKLAGGVAVIKVGAATEVELKEMKLRIEDALNATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 453
B. subtilis gr IVEGAGE---TDKISARVQIRSQIEEST--SEFDREKLQERLAKLAGGVAVIKVGAATEVELKEMKLRIEDALNATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 453
Clostridium h IVNGRGN---SEETKRNINQIKLQLEATT--SEFDREKLQERLAKLAGGVAVIKVGAATEVELKEMKLRIEDALNATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 453
Cowdria hsp60 IIDGVGD---EAAIQGRVQIRSQIEEAT--SDYDREKLQERLAKLAGGVAVIKVGAATEVEHMEKKARVEDALHATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 454
Haemophilus h IIDGVGD---EAAIQGRVQIRSQIEEAT--SDYDREKLQERLAKLAGGVAVIKVGAATEVEHMEKKARVEDALHATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 458
L. pneumophila IIDGVGD---EAAIQGRVQIRSQIEEAT--SDYDREKLQERLAKLAGGVAVIKVGAATEVEHMEKKARVEDALHATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 456
M. avium hsp60 IVEGAGD---SDAIGRAVQIRSQIEEST--SDYDREKLQERLAKLAGGVAVIKVGAATEVELKEMKLRIEDALNATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 455
M. bovis hsp60 IVEGAGD---SDAIGRAVQIRSQIEEST--SDYDREKLQERLAKLAGGVAVIKVGAATEVELKEMKLRIEDALNATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 458
M. leprae groE IVDGGG---SNDVAKRVNQLRAEIEVSD--SEMDREKLQERLAKLAGGVAVIKVGAATEVELKEMKLRIEDALNATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 455
M. leprae hsp6 IVEGAGD---SDAIGRAVQIRSQIEEST--SDYDREKLQERLAKLAGGVAVIKVGAATEVELKEMKLRIEDALNATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 453
M. tuberculosis IIDGVGD---EAAIQGRVQIRSQIEEAT--SDYDREKLQERLAKLAGGVAVIKVGAATEVEHMEKKARVEDALHATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 456
N. meningitidis IIDGVGD---EAAIQGRVQIRSQIEEAT--SDYDREKLQERLAKLAGGVAVIKVGAATEVEHMEKKARVEDALHATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 456
S. aureus hsp6 VVDGGD---ENSDARVQIRSQIEEST--SDYDREKLQERLAKLAGGVAVIKVGAATEVELKEMKLRIEDALNATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 454
Synechocystis IVEAGNE---AAVKSCEQIRSQIEEST--SDYDREKLQERLAKLAGGVAVIKVGAATEVELKEMKLRIEDALNATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 456
Synechocystis LVAGADKRASAGVKEIEQLRKEVAAASD--SDYDREKLQERLAKLAGGVAVIKVGAATEVELKEMKLRIEDALNATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 458
Tsukamurella IVDGAGS---KEQIAGRVQIRSQIEEST--SDYDREKLQERLAKLAGGVAVIKVGAATEVELKEMKLRIEDALNATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 452
S. pombe hsp60 IMKGAGD---VKYNDRCQIRGVMADPNLT--SEYDREKLQERLAKLAGGVAVIKVGAATEVELKEMKLRIEDALNATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 478
S. cerevisiae ILNGSGPK---EATQERIEQIKGSDITTTNSYEKEKLQERLAKLAGGVAVIKVGAATEVELKEMKLRIEDALNATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 488
P. falciparum IMEGGKK---EETNERCESIRNATKMT--SDYDREKLQERLAKLAGGVAVIKVGAATEVELKEMKLRIEDALNATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 483
Onchocerca hs IV--SE--NRVTDVIRKARIEQIKSQIEEST--SDYDREKLQERLAKLAGGVAVIKVGAATEVELKEMKLRIEDALNATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 459
C. elegans-hsp LLRGRGDQ---TEIEKRIEITDEIERST--SDYDREKLQERLAKLAGGVAVIKVGAATEVELKEMKLRIEDALNATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 472
D. melanogaste LLKGKGGK---DDVLRANQIRTKIEDTT--SEYDREKLQERLAKLAGGVAVIKVGAATEVELKEMKLRIEDALNATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 481
human hsp60 LLKGKGGK---AQIEKRIEITDEIERST--SDYDREKLQERLAKLAGGVAVIKVGAATEVELKEMKLRIEDALNATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 481
Arabidopsis h ILDGAGDK---KGIEERCEQIRSAIELST--SDYDREKLQERLAKLAGGVAVIKVGAATEVELKEMKLRIEDALNATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 486
maize hsp60 ILDGAGDK---KSTIEERADQIRSAVENST--SDYDREKLQERLAKLAGGVAVIKVGAATEVELKEMKLRIEDALNATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 489
RUBISCO chape ITADAASK---DELQSRVAQLKELSETD--STYDSEKLQERLAKLAGGVAVIKVGAATEVELKEMKLRIEDALNATRAAVEEGVAGGVALLIRVASKITAGLKQ--NEDQNVGKIKVALRAMESPLRQIVS 503

FIG. 10D



	530	540	550	560	570	580	590	600	610	620	
	NAGLEGSV-VVEKVKV	---SEAG-GYNAATGEYVDMITAAAGIIDPTKVT	RSALQNAASVASLMLTTEAVVVDKPEKEA	APAG-MPGM	---	MGGMGGMGM	---	M---			
<i>S. pneumoniae</i>	NCGEPSV-VANTVKA	---GDGNYGYNAATEEYGNMIDMGIIDPTKVT	RSALQVAASVAGLMITTECMWTDLPKG	DAPDLG-AAG	---	GMGGMG					543
<i>S. pyogenes</i> hs	NAGEPSV-VTNVKA	---GEGNYGYNAATEEYGNMIDMGIIDPTKVT	RSALQVAASVAGLMITTECMWTDLPKG	DAPDLG-AAG	---	MGGMG					544
<i>S. pneumoniae</i>	NAGFESI-VDRLLKN	---AELGIGFNAATGEVNMIDQGIIDPTKVT	RSALQNAASVASILITTEAVVANKPEVAP	APA-M---		DPSMMGGMG					545
<i>S. pyogenes</i> hs	NAGEGSV-VDRLLKN	---SPAGTGFAATGEVNMIDQGIIDPTKVT	RSALQNAASVASILITTEAVVANKPEVAP	APA-M---		MPAGMDPGMMGGMG					546
<i>B. subtilis</i> gr	NAGLEGSV-IVERLKN	---EEIGVGFAATGEVNMIEKGIIDPTKVT	RSALQNAASVAMFLITTEAVVADKPEENG	GAG-MP---		DMGGMGGMGM	---	M			547
<i>Clostridium</i> h	NAGLEGSV-IIEKVKV	---SDAGVGFDALRGEYKDMIKAGIIDPTKVT	RSALQNAASVASTFLITTEAAVDIPEK	---		E-MPQGAGM	---	GMDGM	---	Y	548
<i>Cowdria</i> hsp60	NAGSENAPCVTAHLKQNDKELT	---FNVDTVTNFAFTSGVIDPLKVRIAFDFAV	SLAAMFLITTECMWTDLPKG	DAPDLG-AAG	---	GMGGMG					549
<i>L. pneumophila</i>	NAGEEASV-IASAVKN	---GEGNFGYNAGTEQYGDMIAMGIIDPTKVT	RSALQFAASVAGLMITTECMWTDLPKG	DAPDLG-AAG	---	GMGGMG					550
<i>M. avium</i> hsp60	NAGLEGSV-VNKKVSE	---HKDNYGFAATGEYGDMEVEMGIIDPTKVT	RSALQNAASVASLMLTTECMWTDLPKG	KEEG-VG-		AGDMGGMGGMGM	---	MZ			551
<i>M. bovis</i> hsp60	NSGLEPGV-VAEKVRN	---SPAGTGLNAATGEVEDLLKAGIADP	KVTRSAALQNAASVAGLITTEAVVADKPEKA	APAG-DPTG	---	GMGGMD	---	F			552
<i>M. leprae</i> groE	NAGLEGSV-VAEKVRN	---LPAGHGLNAATGEVEDLLKAGIADP	KVTRSAALQNAASVAGLITTEAVVADKPEKA	VP-G-GG	---	DMGGMD	---	F			553
<i>M. tuberculosis</i>	NAGLEGSV-VAEKVRN	---LSVGHGLNAATGEVEDLLKAGIADP	KVTRSAALQNAASVAGLITTEAVVADKPEKA	VP-G-GG	---	DMGGMD	---	F			554
<i>N. meningitidis</i>	NAGLEGSV-VNKKVSE	---LPAGHGLNAATGEVEDLLKAGIADP	KVTRSAALQNAASVAGLITTEAVVADKPEKA	VP-G-GG	---	DMGGMD	---	F			555
<i>S. aureus</i> hsp60	NAGLEGSV-VNKKVSE	---GKNGYGYNAGSGEYGDMEVEMGIIDPTKVT	RSALQHAASVAGLITTECMWTDLPKG	DAPDLG-AAG	---	GMGGMG					556
<i>Synechocystis</i>	NAGQNGAV-ISERVKE	---KEFNVGYNAASLEYVDMLAAGIIDPTKVT	RSALQNAASVAGLITTECMWTDLPKG	DAPDLG-AAG	---	GMGGMG					557
<i>Synechocystis</i>	NAGLEGSV-IVERLKN	---AEPGVGFNGATNEWMMLRGIIDPTKVT	RSALQHAASVAMFLITTEAVVANKPEVAP	APA-M---		MPAGMDPGMMGGMG					558
<i>Tsukamurella</i>	NAGLEGSV-IVERLKN	---ATGNQGYNVITGKIIDLAAAGIIDPTKVT	RSALQNAASVAGLITTECMWTDLPKG	DAPDLG-AAG	---	GMGGMG					559
<i>S. pombe</i> hsp60	NAGLEGNL-IVGKLKELYGKEFNIGYDI	AKDRFVDLNETGLDPLKVRIAFDFAVSLA	AMFLITTECMWTDLPKG	DAPDLG-AAG	---	GMGGMG					560
<i>S. cerevisiae</i>	NAGEGSV-IIGKLI	DEYGDFAKGYDASKSEYTDMLATGIIDPTKVT	RSALQNAASVAGLITTECMWTDLPKG	DAPDLG-AAG	---	GMGGMG					561
<i>P. falciparum</i>	NAGLEGSV-VNKKVSE	---GKNGYGYNAGSGEYGDMEVEMGIIDPTKVT	RSALQHAASVAGLITTECMWTDLPKG	DAPDLG-AAG	---	GMGGMG					562
<i>Onchocerca</i> hs	NAGLEGSV-IIGKLI	DEYGDFAKGYDASKSEYTDMLATGIIDPTKVT	RSALQNAASVAGLITTECMWTDLPKG	DAPDLG-AAG	---	GMGGMG					563
<i>C. elegans</i> hsp	NAGLEPSV-IIDEVTSNTSY	---GYDALNGKFDVDMFEAGIIDPTKVT	RSALQNAASVAGLITTECMWTDLPKG	DAPDLG-AAG	---	GMGGMG					564
<i>D. melanogaster</i>	NAGVDGAM-VVAKVENOAG-DY	---GYDA-KGEYGNLIEKGIIDPTKVT	RSALQNAASVAGLITTECMWTDLPKG	DAPDLG-AAG	---	GMGGMG					565
<i>human</i> hsp60	NAGVEGSL-IVEKIM-QSSSEV	---GYDAMAGDFVNMVEKGIIDPTKVT	RSALQNAASVAGLITTECMWTDLPKG	DAPDLG-AAG	---	GMGGMG					566
<i>Arabidopsis</i> h	NAGVEGAV-IVGKLLEQNDPL	---GYDAKGEYVDMVKAGIIDPLK	VRTALVDAASVSLITTEAVVVDLPK	DESESGAA-GG	---	GMGGMG					567
<i>maize</i> hsp60	NAGVEGAV-VVGKLLEQNDPL	---GYDAKGEYVDMVKAGIIDPLK	VRTALVDAASVSLITTEAVVVDLPK	DESESGAA-GG	---	GMGGMG					568
<i>RUBISCO</i> chape	NAGIEGEV-VVEKIKV	---GEMEYGYNANTDTYENLVESGVID	PAKVT	RSALQNAASVAGLITTECMWTDLPKG	DAPDLG-AAG	---	GMGGMG				569

FIG. 10E

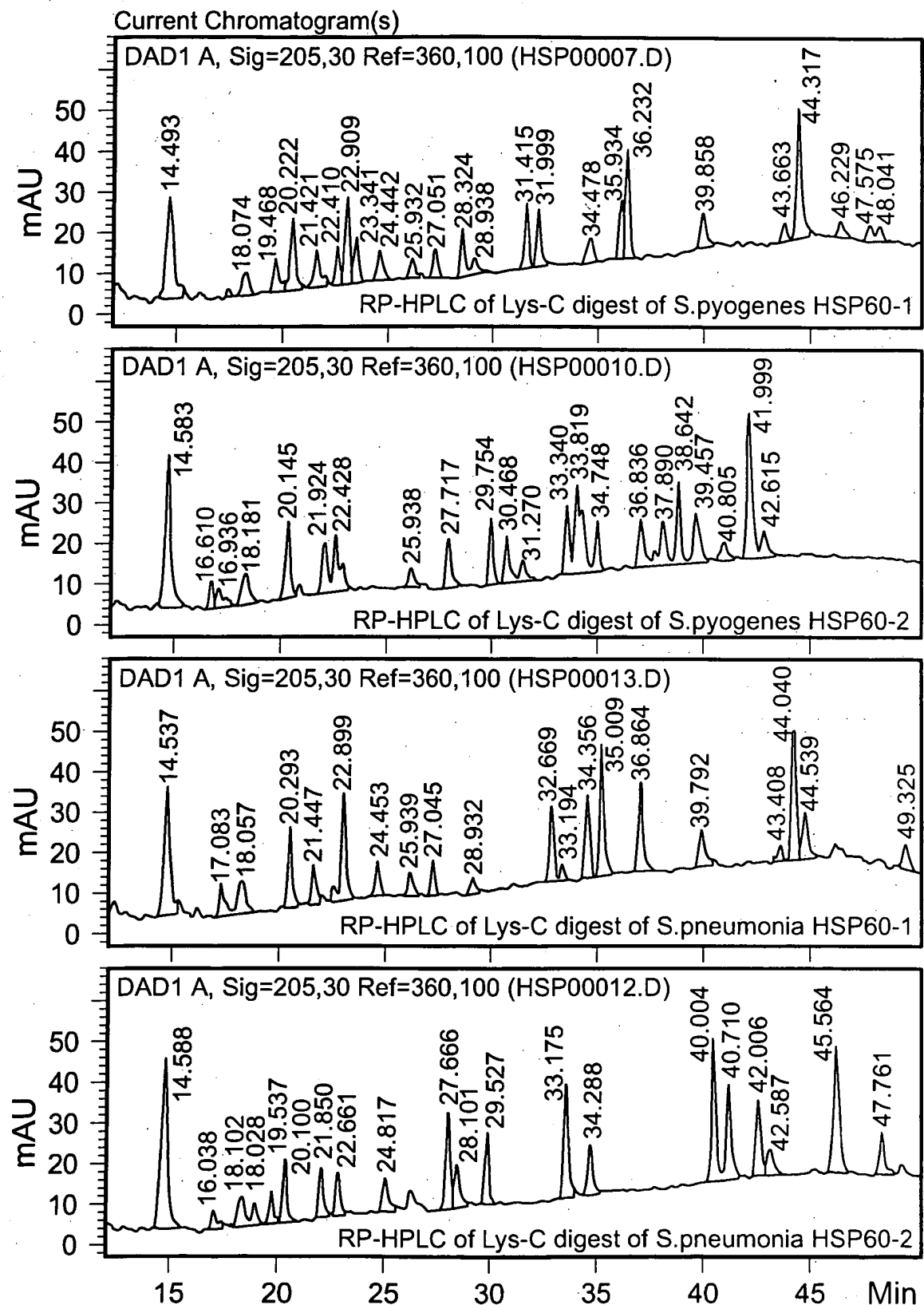


FIG. 11